

(1) GENERAL INFORMATION

- (ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL TRACT
- (iii) NUMBER OF SEQUENCES: 22
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Abbott Laboratories
 - (B) STREET: 100 Abbott Park Road
 - (C) CITY: Abbott Park
 - (D) STATE: IL
 - (E) COUNTRY: USA
 - (F) ZIP: 60064-3500
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/828,845
 - (B) FILING DATE: 31-MAR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Becker, Cheryl L.
 - (B) REGISTRATION NUMBER: 35,441
 - (C) REFERENCE/DOCKET NUMBER: 6066.US.P1
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 847/935-1729
 - (B) TELEFAX: 847/938-2623
 - (C) TELEX:

- (A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:1:

CTGGGATCAG	CCACTGCAGC	TCCCTGAGCA	CTCTCTACAG	AGACGCGGAC	CCCAGACATG	60
AGGAGGCTCC	TCCTGGTCAC	CAGCCTGGTG	GTTGTGCTGC	TGTGGGAGGC	AGGTGCAGTC	120
CCAGCACCCA	AGGTCCCTAT	CAAGATGCAA	GTCAAACACT	GGCCCTCAGA	GCAGGACCCA	180
GAGAAGGCCCT	GGGGCGCCCG	TGTGGTGGAG	CCTCCGGAGA	AGGACGACCA	GCTGGTGGTG	240
CTGTTCCCTG	TCCA					254

(2) INFORMATION FOR SEO ID NO:2:

- (A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGCCACTGCA	GCTCCCTGAG	CACTCTCTAC	AGAGACGCGG	ACCCAGACA	TGAGGAGGCT	60
CCTCCTGGTC	ACCAGCCTGG	TGGTTGTGCT	GCTGTGGGAG	GCAGGTGCAG	TCCCAGCACC	120
CAAGGTCCCT	ATCAAGATCA	AAGTCAAACA	CTGGCCCTCA	GAGCAGGACC	CAGAGAAGGC	180
CTGGGGCGCC	CGTGTGGTGG	AGCCTCCGGA	GAAGGACGAC	CAGCTGGTGG	TGCTGTTCCC	240
TGTCCAGAAG	CCGAAACTCT	T				261

(2) INFORMATION FOR SEO ID NO:3:

- (A) LENGTH: 534 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
(B) LOCATION: 458
(D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCCCGGCCTG	CTGGGGTTTA	TTTGTCTAGC	TGGGGCAGGG	TAGGGAGGGT	CCCAGTCCCA	60
ACAGCCCTGGG	CCTTGGGACA	GGGCGGGGGC	AGTGATGGCC	CCTGGAGCCC	TACTGGGGGT	120
GGTAGATGTG	GTCTTGGTCT	TCCTCGGGTC	CCAGGAGCAC	CTGGTGATT	GGCATCACCC	180
ACAACCGGGG	CTCTCCTCG	CCCTGGTCTT	CCTCAGGCGG	AGGGTGATTAC	AGGCTGTCTAT	240
GGTCGGGCTC	GGGACTCAGG	ACACGGCCCA	GGGTGTCCTC	GGTCTCCATC	CAGGCCTTGG	300
TGCCTGGAAG	GATGGGGCCC	CTGCCCTGAC	CTCGTGGCTT	CTCCTCGGTG	GTCAAGAGTT	360
TCGGCTTCTG	GACAGGGAAC	AGCACCCACA	GCTGGTGCCT	CTTCTCCGGA	GGCTCCACCA	420
CACGGCGCGC	CAGGCTTCT	CTGGGTCTCT	CTCTGAGNGG	CAGTGTTTGA	CTTGCATCTT	480
GATAGGGAAC	TTGGGTGCTG	GGAATGCACC	TGCCTCCCAC	AGAAAAA	CAAC	534

(2) INFORMATION FOR SEQ ID NO:4:

- (A) LENGTH: 615 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGCCACTGCA	GCTCCCTGAG	CACTCTCTAC	AGAGACGCGG	ACCCAGACA	TGAGGAGGCT	60
CCTCCTGGTC	ACCAGCCTGG	TGGTTGTGCT	GCTGTGGGAG	GCAGGTGCAG	TCCCAGCACC	120
CAAGGTCCCT	ATCAAGATGC	AAGTCAAACA	CTGGCCCTCA	GAGCAGGACC	CAGAGAAGGC	180
CTGGGGCGCC	CGTGTGGTGG	AGCCTCCGGA	GAAGGACGAC	CAGCTGGTGG	TGCTGTTCCC	240
TGTCCAGAAG	CCGAAACTCT	TGACCACCGA	GGAGAAGCCA	CGAGGTCAGG	GCAGGGGCCC	300
CATCCTTCCA	GGCACCAAGG	CCTGGATGGA	GACCGAGGAC	ACCCTGGGCC	GTGTCCTGAG	360
TCCCGAGCCC	GACCATGACA	GCCTGTACCA	CCCTCCGCCT	GAGGAGGACC	AGGGCGAGGA	420
GAGGCCCCGG	TTGTGGGTGA	TGCCAAATCA	CCAGGTGCTC	CTGGGACCGG	AGGAAGACCA	480
AGACCACATC	TACCACCCCC	AGTAGGGCTC	CAGGGGCCAT	CACTGCCCCC	GCCCTGTCCC	540
AAGGCCCAGG	CTGTTGGGAC	TGGGACCCTC	CCTACCCTGC	CCCAGCTAGA	CAAATAAACC	600
CCAGCAGGCC	GGGCA					615

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 622 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGGGATCAG	CCACTGCAGC	TCCCTGAGCA	CTCTCTACAG	AGACGCGGAC	CCCAGACATG	60
AGGAGGCTCC	TCCTGGTCAC	CAGCCTGGTG	GTTGTGCTGC	TGTGGGAGGC	AGGTGCAGTC	120
CCAGCACCCA	AGGTCCCTAT	CAAGATGCAA	GTCAAACACT	GGCCCTCAGA	GCAGGACCCA	180
GAGAAGGCCT	GGGGCGCCCG	TGTGGTGGAG	CCTCCGGAGA	AGGACGACCA	GCTGGTGGTG	240
CTGTTCCCTG	TCCAGAAGCC	GAAACTCTTG	ACCACCGAGG	AGAAGCCACG	AGGTCAGGGC	300
AGGGGCCCCA	TCCTTCCAGG	CACCAAGGCC	TGGATGGAGA	CCGAGGACAC	CCTGGGCCGT	360
GTCCTGAGTC	CCGAGCCCCA	CCATGACAGC	CTGTACCACC	CTCCGCCTGA	GGAGGACCAG	420
GGCGAGGAGA	GGCCCCGTT	GTGGGTGATG	CCAAATCACC	AGGTGCTCCT	GGGACCGGAG	480
GAAGACCAAG	ACCACATCTA	CCACCCCCAG	TAGGGCTCCA	GGGGCCATCA	CTGCCCCCGC	540
CCTGTCCCAA	GGCCAGGCT	GTTGGGACTG	GGACCCTCCC	TACCCTGCCC	CAGCTAGACA	600
AATAAACCCC	AGCAGGCCGG	GA				622

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGCTCGGAAT	TCCGAGCTTG	GATCCTCTAG	AGCGGCCGCC	GACTAGTGAG	CTCGTCGACC	60
CGGGAATT						68

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

0904995 0904995 0904995

AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG
GAATTCCG

60
68

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGCGGATAAC AATTCACAC AGGA

24

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGTAAAACGA CGGCCAGT

18

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTGTCCAGAA GCCGAAACTC

20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGGAAGACCA AGACCACATC

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

BBZLF0"55354060

GGTAGATGTG GTCTTGGTCT TC

22

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTCGGTGGTC AAGAGTTTCG

20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTCCCTGTCC AGAAGCCGAA ACTC

24

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGGGGTTTAT TTGTCTAGCT GGGGC

25

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met	Arg	Arg	Leu	Leu	Leu	Val	Thr	Ser	Leu	Val	Val	Val	Leu	Leu	Trp
1				5					10				15		
Glu	Ala	Gly	Ala	Val	Pro	Ala	Pro	Lys	Val	Pro	Ile	Lys	Met	Gln	Val
			20					25				30			
Lys	His	Trp	Pro	Ser	Glu	Gln	Asp	Pro	Glu	Lys	Ala	Trp	Gly	Ala	Arg
		35				40					45				
Val	Val	Glu	Pro	Pro	Glu	Lys	Asp	Asp	Gln	Leu	Val	Val	Leu	Phe	Pro
	50					55				60					
Val	Gln	Lys	Pro	Lys	Leu	Leu	Thr	Thr	Glu	Glu	Lys	Pro	Arg	Gly	Gln
65					70				75					80	
Gly	Arg	Gly	Pro	Ile	Leu	Pro	Gly	Thr	Lys	Ala	Trp	Met	Glu	Thr	Glu
			85						90					95	

Asp Thr Leu Gly Arg Val Leu Ser Pro Glu Pro Asp His Asp Ser Leu
 100 105 110
 Tyr His Pro Pro Pro Glu Glu Asp Gln Gly Glu Glu Arg Pro Arg Leu
 115 120 125
 Trp Val Met Pro Asn His Gln Val Leu Leu Gly Pro Glu Glu Asp Gln
 130 135 140
 Asp His Ile Tyr His Pro Gln
 145 150

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gly Ala Val Pro Ala Pro Lys Val Pro Ile Lys Met Gln Val Lys His
 1 5 10 15
 Trp Pro Ser Glu Gln Asp Pro Glu Lys Ala Trp Gly Ala
 20 25

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Arg Val Val Glu Pro Pro Glu Lys Asp Asp Gln Leu Val Val Leu Phe
 1 5 10 15
 Pro Val Gln Lys Pro Lys Leu Leu Thr Thr Glu Glu Lys Pro Arg Gly
 20 25 30
 Gln Gly Arg Gly
 35

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Leu Pro Gly Thr Lys Ala Trp Met Glu Thr Glu Asp Thr Leu Gly Arg
 1 5 10 15
 Val Leu Ser Pro Glu Pro Asp His Asp Ser Leu Tyr His Pro Pro Pro
 20 25 30
 Glu Glu Asp
 35

(2) INFORMATION FOR SEQ ID NO:20:

09049695-032798

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Pro	Glu	Glu	Asp	Gln	Gly	Glu	Glu	Arg	Pro	Arg	Leu	Trp	Val	Met	Pro
1				5				10						15	
Asn	His	Gln	Val	Leu	Leu	Gly	Pro	Glu	Glu	Asp	Gln	Asp	His	Ile	Tyr
			20				25						30		

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys
1				5			

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Met	His	Thr	Glu	His
1				5				10						15	
His	His	His	His	His											
				20											

03049699, 032798